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RAW SEQUENCE LISTING

DATE: 02/27/2003

PATENT APPLICATION: US/09/857,123A

TIME: 10:56:32

Input Set : A:\Pg3606SEQLST.txt

Output Set: N:\CRF4\02272003\I857123A.raw

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4 <110> APPLICANT: Glaxo Group Ltd
5     Tate, Simon N
6     Delany, Natalie S
7     Sanseau, P
9 <120> TITLE OF INVENTION: Novel Receptors
11 <130> FILE REFERENCE: PG3606
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/857,123A
C--> 14 <141> CURRENT FILING DATE: 2000-06-01
16 <150> PRIOR APPLICATION NUMBER: GB 9826359.3
17 <151> PRIOR FILING DATE: 1998-12-01
19 <160> NUMBER OF SEQ ID NOS: 40
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 4365
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
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29 <221> NAME/KEY: CDS
30 <222> LOCATION: (775)..(3294)
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37 tgtataagct cagtggctgt ggcagcgagg ttgaagagca aaggcaggcc gggcacctgg 180
40 ctgatgatgt gtggaccctg tgcacagcag ggcccgcagt gcggtgtggg tgtgggtggg 240
42 ccagtctctg ccgctcacc ctttccaggg acacagtctg cttggctctt ctggactgag 300
44 ccatacctcat caccgagatc ctccctgaat tcagcccacg acagccaccc cggccgtttt 360
46 ccttgttctg tgtgggaagg gaggcagcgc ggtggttatc aacctcacc tgcagaggag 420
48 gcacctgagg cccagagacg aggagggatg ggtctaacc agaaccacag atggctctga 480
50 gccggggggc tgtccaccct cccaggccga cgtcagtggc cgcaggactg cctgggccc 540
52 gctaggcctg ctacacctg aggccctctg ggtgagaggt tcagtcctgg aaacacttca 600
54 gttctagggg gctgggggca gcagcaagtt ggagttttgg ggtaccctgc ttcacagggc 660
56 ccttggaag gagggcagg ggggtctaag gacaagcagt ccttactttg ggagtcaacc 720
58 ccggcgtggt ggctgctgca ggttgcacac tgggccacag aggatccagc aagg atg 777
59                                     Met
60                                     1
62 aag aaa tgg agc agc aca gac ttg ggg gca gct gcg gac cca ctc caa 825
63 Lys Lys Trp Ser Ser Thr Asp Leu Gly Ala Ala Ala Asp Pro Leu Gln
64         5                10                15
66 aag gac acc tgc cca gac ccc ctg gat gga gac cct aac tcc agg cca 873
67 Lys Asp Thr Cys Pro Asp Pro Leu Asp Gly Asp Pro Asn Ser Arg Pro
68         20                25                30
70 cct cca gcc aag ccc cag ctc tcc acg gcc aag agc cgc acc cgg ctc 921
71 Pro Pro Ala Lys Pro Gln Leu Ser Thr Ala Lys Ser Arg Thr Arg Leu

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75	Phe Gly Lys Gly Asp Ser Glu Glu Ala Phe Pro Val Asp Cys Pro His			
76	50 55 60 65			
79	gag gaa ggt gag ctg gac tcc tgc ccg acc atc aca gtc agc cct gtt	1017		
80	Glu Glu Gly Glu Leu Asp Ser Cys Pro Thr Ile Thr Val Ser Pro Val			
81	70 75 80			
83	atc acc atc cag agg cca gga gac ggc ccc acc ggt gcc agg ctg ctg	1065		
84	Ile Thr Ile Gln Arg Pro Gly Asp Gly Pro Thr Gly Ala Arg Leu Leu			
85	85 90 95			
87	tcc cag gac tct gtc gcc gcc agc acc gag aag acc ctc agg ctc tat	1113		
88	Ser Gln Asp Ser Val Ala Ala Ser Thr Glu Lys Thr Leu Arg Leu Tyr			
89	100 105 110			
91	gat cgc agg agt atc ttt gaa gcc gtt gct cag aat aac tgc cag gat	1161		
92	Asp Arg Arg Ser Ile Phe Glu Ala Val Ala Gln Asn Asn Cys Gln Asp			
93	115 120 125			
95	ctg gag agc ctg ctg ctc ttc ctg cag aag agc aag aag cac ctc aca	1209		
96	Leu Glu Ser Leu Leu Leu Phe Leu Gln Lys Ser Lys Lys His Leu Thr			
97	130 135 140 145			
99	gac aac gag ttc aaa gac cct gag aca ggg aag acc tgt ctg ctg aaa	1257		
100	Asp Asn Glu Phe Lys Asp Pro Glu Thr Gly Lys Thr Cys Leu Leu Lys			
101	150 155 160			
103	gcc atg ctc aac ctg cac gac gga cag aac acc acc atc ccc ctg ctc	1305		
104	Ala Met Leu Asn Leu His Asp Gly Gln Asn Thr Thr Ile Pro Leu Leu			
105	165 170 175			
107	ctg gag atc gcg cgg caa acg gac agc ctg aag gag ctt gtc aac gcc	1353		
108	Leu Glu Ile Ala Arg Gln Thr Asp Ser Leu Lys Glu Leu Val Asn Ala			
109	180 185 190			
111	agc tac acg gac agc tac tac aag ggc cag aca gca ctg cac atc gcc	1401		
112	Ser Tyr Thr Asp Ser Tyr Tyr Lys Gly Gln Thr Ala Leu His Ile Ala			
113	195 200 205			
116	atc gag aga cgc aac atg gcc ctg gtg acc ctc ctg gtg gag aac gga	1449		
117	Ile Glu Arg Arg Asn Met Ala Leu Val Thr Leu Leu Val Glu Asn Gly			
118	210 215 220 225			
120	gca gac gtc cag gct gcg gcc cat ggg gac ttc ttt aag aaa acc aaa	1497		
121	Ala Asp Val Gln Ala Ala Ala His Gly Asp Phe Phe Lys Lys Thr Lys			
122	230 235 240			
124	ggg cgg cct gga ttc tac ttc ggt gaa ctg ccc ctg tcc ctg gcc gcg	1545		
125	Gly Arg Pro Gly Phe Tyr Phe Gly Glu Leu Pro Leu Ser Leu Ala Ala			
126	245 250 255			
128	tgc acc aac cag ctg ggc atc gtg aag ttc ctg ctg cag aac tcc tgg	1593		
129	Cys Thr Asn Gln Leu Gly Ile Val Lys Phe Leu Leu Gln Asn Ser Trp			
130	260 265 270			
132	cag acg gcc gac atc agc gcc agg gac tcg gtg ggc aac acg gtg ctg	1641		
133	Gln Thr Ala Asp Ile Ser Ala Arg Asp Ser Val Gly Asn Thr Val Leu			
134	275 280 285			
136	cac gcc ctg gtg gag gtg gcc gac aac acg gcc gac aac acg aag ttt	1689		
137	His Ala Leu Val Glu Val Ala Asp Asn Thr Ala Asp Asn Thr Lys Phe			
138	290 295 300 305			

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140 gtg acg agc atg tac aat gag att ctg atc ctg ggg gcc aaa ctg cac 1737
141 Val Thr Ser Met Tyr Asn Glu Ile Leu Ile Leu Gly Ala Lys Leu His
142 310 315 320
144 ccg acg ctg aag ctg gag gag ctc acc aac aag aag gga atg acg ccg 1785
145 Pro Thr Leu Lys Leu Glu Glu Leu Thr Asn Lys Lys Gly Met Thr Pro
146 325 330 335
148 ctg gct ctg gca gct ggg acc ggg aag atc ggg gtc ttg gcc tat att 1833
149 Leu Ala Leu Ala Ala Gly Thr Gly Lys Ile Gly Val Leu Ala Tyr Ile
150 340 345 350
153 ctc cag cgg gag atc cag gag ccc gag tgc agg cac ctg tcc agg aag 1881
154 Leu Gln Arg Glu Ile Gln Glu Pro Glu Cys Arg His Leu Ser Arg Lys
155 355 360 365
157 ttc acc gag tgg gcc tac ggg ccc gtg cac tcc tcg ctg tac gac ctg 1929
158 Phe Thr Glu Trp Ala Tyr Gly Pro Val His Ser Ser Leu Tyr Asp Leu
159 370 375 380 385
161 tcc tgc atc gac acc tgc gag aag aac tcg gtg ctg gag gtg atc gcc 1977
162 Ser Cys Ile Asp Thr Cys Glu Lys Asn Ser Val Leu Glu Val Ile Ala
163 390 395 400
165 tac agc agc agc gag acc cct aat cgc cac gac atg ctc ttg gtg gag 2025
166 Tyr Ser Ser Ser Glu Thr Pro Asn Arg His Asp Met Leu Leu Val Glu
167 405 410 415
169 ccg ctg aac cga ctc ctg cag gac aag tgg gac aga ttc gtc aag cgc 2073
170 Pro Leu Asn Arg Leu Leu Gln Asp Lys Trp Asp Arg Phe Val Lys Arg
171 420 425 430
173 atc ttc tac ttc aac ttc ctg gtc tac tgc ctg tac atg atc atc ttc 2121
174 Ile Phe Tyr Phe Asn Phe Leu Val Tyr Cys Leu Tyr Met Ile Ile Phe
175 435 440 445
177 acc atg gct gcc tac tac agg ccc gtg gat ggc ttg cct ccc ttt aag 2169
178 Thr Met Ala Ala Tyr Tyr Arg Pro Val Asp Gly Leu Pro Pro Phe Lys
179 450 455 460 465
181 atg gaa aaa att gga gac tat ttc cga gtt act gga gag atc ctg tct 2217
182 Met Glu Lys Ile Gly Asp Tyr Phe Arg Val Thr Gly Glu Ile Leu Ser
183 470 475 480
185 gtg tta gga gga gtc tac ttc ttt ttc cga ggg att cag tat ttc ctg 2265
186 Val Leu Gly Gly Val Tyr Phe Phe Phe Arg Gly Ile Gln Tyr Phe Leu
187 485 490 495
190 cag agg cgg ccg tcg atg aag acc ctg ttt gtg gac agc tac agt gag 2313
191 Gln Arg Arg Pro Ser Met Lys Thr Leu Phe Val Asp Ser Tyr Ser Glu
192 500 505 510
194 atg ctt ttc ttt ctg cag tca ctg ttc atg ctg gcc acc gtg gtg ctg 2361
195 Met Leu Phe Phe Leu Gln Ser Leu Phe Met Leu Ala Thr Val Val Leu
196 515 520 525
198 tac ttc agc cac ctc aag gag tat gtg gct tcc atg gta ttc tcc ctg 2409
199 Tyr Phe Ser His Leu Lys Glu Tyr Val Ala Ser Met Val Phe Ser Leu
200 530 535 540 545
202 gcc ttg ggc tgg acc aac atg ctc tac tac acc cgc ggt ttc cag cag 2457
203 Ala Leu Gly Trp Thr Asn Met Leu Tyr Tyr Thr Arg Gly Phe Gln Gln
204 550 555 560
206 atg ggc atc tat gcc gtc atg ata gag aag atg atc ctg aga gac ctg 2505

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210	tgc	cgt	ttc	atg	ttt	gtc	tac	atc	gtc	ttc	ttg	ttc	ggg	ttt	tcc	aca	2553
211	Cys	Arg	Phe	Met	Phe	Val	Tyr	Ile	Val	Phe	Leu	Phe	Gly	Phe	Ser	Thr	
212			580						585					590			
214	gcg	gtg	gtg	acg	ctg	att	gaa	gac	ggg	aag	aat	gac	tcc	ctg	ccg	tct	2601
215	Ala	Val	Val	Thr	Leu	Ile	Glu	Asp	Gly	Lys	Asn	Asp	Ser	Leu	Pro	Ser	
216			595					600					605				
218	gag	tcc	acg	tcg	cac	agg	tgg	cgg	ggg	cct	gcc	tgc	agg	ccc	ccc	gat	2649
219	Glu	Ser	Thr	Ser	His	Arg	Trp	Arg	Gly	Pro	Ala	Cys	Arg	Pro	Pro	Asp	
220	610					615					620					625	
222	agc	tcc	tac	aac	agc	ctg	tac	tcc	acc	tgc	ctg	gag	ctg	ttc	aag	ttc	2697
223	Ser	Ser	Tyr	Asn	Ser	Leu	Tyr	Ser	Thr	Cys	Leu	Glu	Leu	Phe	Lys	Phe	
224				630						635					640		
227	acc	atc	ggc	atg	ggc	gac	ctg	gag	ttc	act	gag	aac	tat	gac	ttc	aag	2745
228	Thr	Ile	Gly	Met	Gly	Asp	Leu	Glu	Phe	Thr	Glu	Asn	Tyr	Asp	Phe	Lys	
229				645						650					655		
231	gct	gtc	ttc	atc	atc	ctg	ctg	ctg	gcc	tat	gta	att	ctc	acc	tac	atc	2793
232	Ala	Val	Phe	Ile	Ile	Leu	Leu	Leu	Ala	Tyr	Val	Ile	Leu	Thr	Tyr	Ile	
233			660						665					670			
235	ctc	ctg	ctc	aac	atg	ctc	atc	gcc	ctc	atg	ggt	gag	act	gtc	aac	aag	2841
236	Leu	Leu	Leu	Asn	Met	Leu	Ile	Ala	Leu	Met	Gly	Glu	Thr	Val	Asn	Lys	
237			675				680						685				
239	atc	gca	cag	gag	agc	aag	aac	atc	tgg	aag	ctg	cag	aga	gcc	atc	acc	2889
240	Ile	Ala	Gln	Glu	Ser	Lys	Asn	Ile	Trp	Lys	Leu	Gln	Arg	Ala	Ile	Thr	
241	690					695					700					705	
243	atc	ctg	gac	acg	gag	aag	agc	ttc	ctt	aag	tgc	atg	agg	aag	gcc	ttc	2937
244	Ile	Leu	Asp	Thr	Glu	Lys	Ser	Phe	Leu	Lys	Cys	Met	Arg	Lys	Ala	Phe	
245				710						715					720		
247	cgc	tca	ggc	aag	ctg	ctg	cag	gtg	ggg	tac	aca	cct	gat	ggc	aag	gac	2985
248	Arg	Ser	Gly	Lys	Leu	Leu	Gln	Val	Gly	Tyr	Thr	Pro	Asp	Gly	Lys	Asp	
249				725						730					735		
251	gac	tac	cgg	tgg	tgc	ttc	agg	gtg	gac	gag	gtg	aac	tgg	acc	acc	tgg	3033
252	Asp	Tyr	Arg	Trp	Cys	Phe	Arg	Val	Asp	Glu	Val	Asn	Trp	Thr	Thr	Trp	
253			740						745					750			
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256	Asn	Thr	Asn	Val	Gly	Ile	Ile	Asn	Glu	Asp	Pro	Gly	Asn	Cys	Glu	Gly	
257			755				760						765				
259	gtc	aag	cgc	acc	ctg	agc	ttc	tcc	ctg	cgg	tca	agc	aga	gtt	tca	ggc	3129
260	Val	Lys	Arg	Thr	Leu	Ser	Phe	Ser	Leu	Arg	Ser	Ser	Arg	Val	Ser	Gly	
261	770					775					780					785	
264	aga	cac	tgg	aag	aac	ttt	gcc	ctg	gtc	ccc	ctt	tta	aga	gag	gca	agt	3177
265	Arg	His	Trp	Lys	Asn	Phe	Ala	Leu	Val	Pro	Leu	Leu	Arg	Glu	Ala	Ser	
266				790						795					800		
268	gct	cga	gat	agg	cag	tct	gct	cag	ccc	gag	gaa	gtt	tat	ctg	cga	cag	3225
269	Ala	Arg	Asp	Arg	Gln	Ser	Ala	Gln	Pro	Glu	Glu	Val	Tyr	Leu	Arg	Gln	
270				805						810					815		
272	ttt	tca	ggg	tct	ctg	aag	cca	gag	gac	gct	gag	gtc	ttc	aag	agt	cct	3273
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277 Ala Ala Ser Gly Glu Lys
278      835
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282 cagcctggcc tggctctgtgc ctgcccagca tgttcccaaa tctgtgctgg acaagctgtg 3444
284 ggaagcgttc ttggaagcat ggggagtgat gtacatccaa ccgtcactgt cccaagtga 3504
286 atctcctaac agactttcag gtttttactc actttactaa acagtgttga tggtcagtct 3564
288 ctactgggac atgttaggcc cttgttttct ttgattttat tcttttctgt gagacagagt 3624
290 tctactcttg tggccaggct ggagtgcatg ggtgtgatct tggctcactg caacctctgc 3684
292 tcccgggttc aagcgattct tctgcttcag tctcccaagt agcttggatt acaggtgagc 3744
294 actaccacgc ccgctaatt tttgtatttt taatagagac ggggtttcac catgttggcc 3804
296 aggtctgtct cgaactcttg acctcaggtg atctgccgcg cttggcctcc caaagtgtctg 3864
298 ggattacagg tgtgagccgc tgcgctcggc cttctttgat tttatattat taggagcaaa 3924
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307 caagctgttg cagcagtgcc ttcttcatcc ttcttacga tcaatcacag tctccagaag 4164
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311 gaatgtttga aagatcttcc atttctagga accccagtcg tgcttctccg caatggcaca 4284
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315 aaaaaaaaaa aaaaaaaaaa a                                     4365
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327 Gln Lys Asp Thr Cys Pro Asp Pro Leu Asp Gly Asp Pro Asn Ser Arg
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331 35 40 45
333 Leu Phe Gly Lys Gly Asp Ser Glu Glu Ala Phe Pro Val Asp Cys Pro
334 50 55 60
336 His Glu Glu Gly Glu Leu Asp Ser Cys Pro Thr Ile Thr Val Ser Pro
337 65 70 75 80
339 Val Ile Thr Ile Gln Arg Pro Gly Asp Gly Pro Thr Gly Ala Arg Leu
340 85 90 95
342 Leu Ser Gln Asp Ser Val Ala Ala Ser Thr Glu Lys Thr Leu Arg Leu
343 100 105 110
345 Tyr Asp Arg Arg Ser Ile Phe Glu Ala Val Ala Gln Asn Asn Cys Gln
346 115 120 125
348 Asp Leu Glu Ser Leu Leu Leu Phe Leu Gln Lys Ser Lys Lys His Leu
349 130 135 140
351 Thr Asp Asn Glu Phe Lys Asp Pro Glu Thr Gly Lys Thr Cys Leu Leu
352 145 150 155 160
354 Lys Ala Met Leu Asn Leu His Asp Gly Gln Asn Thr Thr Ile Pro Leu
355 165 170 175

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L:13 M:270 C: Current Application Number differs, Replaced Application Number

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date